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(54) Title: *LACTOBACILLI* HARBORING AGGREGATION AND MUCIN BINDING GENES AS VACCINE DELIVERY VEHICLES

(57) Abstract

Live vaccines and methods for preparing the vaccines useful in protecting a host from infection by a pathogenic microorganism are provided. Vaccines are prepared from live *Lactobacillus* cells which have been transformed using DNA technology to express heterologous antigens of pathogenic microorganisms or other suitable biological material. Genes encoding antigenic determinants pathogenic in the mammalian gastrointestinal tract are inserted into expression cassettes and fused with genes encoding an aggregation factor and/or a mucin binding factor. The inserted genes are shown to transform *L. reuteri* cells. The aggregation enhancing and mucin binding genes have been isolated and sequenced. The vaccine can be ingested orally in a pharmaceutical carrier or in milk products.

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LACTOBACILLI HARBORING AGGREGATION AND MUCIN BINDING GENES AS VACCINE DELIVERY VEHICLES

Field of the Invention

This invention relates to the use of transformed *Lactobacillus* species and in a particular example, *Lactobacillus reuteri* (*L. reuteri*) as vaccine delivery vehicles. Transformed *L. reuteri* are demonstrated to express on their cell surface or to secrete an epitope of an antigen obtained from pathogenic microorganisms. In one embodiment, a gene (*agg*) encoding an aggregation protein and/or a gene (*muc*) encoding a mucin binding protein is fused to a gene encoding an exogenous antigen and used to transform *Lactobacilli*. The exogenous antigen attached to an aggregation protein or a mucin binding protein is expressed on the surface of the cell or secreted into its surroundings. *Lactobacilli*, and in particular *L. reuteri*, are highly effective in targeting the mucosa, such as the gastrointestinal tract or nasal passages, and when transformed as described herein, are effective in provoking a desired immune response against the presenting antigen in the host animal.

Background of the Invention

Lactic acid bacteria have long been used as preservatives for food such as fermented milk, meat, fish, vegetables and cheese and in animal feed. Fermented foods are known to have beneficial effects on the human intestinal environment. *Lactobacillus* species are also useful as probiotics, microorganisms that have beneficial effects in the intestine and promote health when ingested.

Vaccines delivered orally are more convenient than the more commonly used parenteral delivery system, especially when vaccines are to be administered to large numbers of people or animals in less industrialized countries. Earlier attempts to develop oral vaccines have utilized pathogenic organisms, such as *Salmonella* species, as antigen carriers for oral immunization. However, even when these pathogens are attenuated they may pose a danger of reverting to pathogenicity and being harmful to the host animal. Lactic acid bacteria, in general, and *Lactobacillus* species in particular, possess certain properties that make them attractive candidates for use in oral vaccination. These properties of *Lactobacillus* include adjuvant activity, mucosal adhesive properties, and low intrinsic immunogenicity. They are generally regarded as safe (GRAS) as they are present in the animal's endogenous intestinal flora and are used commercially in the production of yogurts, cultured milks and other foods. *Lactobacillus* species are known to be difficult to transform with new genetic information. Those unable to be transformed are referred to as recalcitrants.

The gastrointestinal tract of animals is a complex ecosystem harboring an estimated 300 to 500 species of microorganisms. Despite over 100 years of intensive research in the field of intestinal microbiology, much remains to be learned about these microorganisms. Complex inter-relationships exist among different species of microorganisms and between resident microorganisms and their hosts.

An important factor concerning the utility of *Lactobacillus* species as a vaccine delivery vehicle is their ability to adhere to the epithelial cells of the animal to be vaccinated. Knowledge of the structure and mode of expression of surface related proteins of *Lactobacillus* that are involved in adherence to mucosal tissues and/or the extra-cellular matrix is important in designing an effective vaccination system. Adherence factors can be

critical to proper antigen presentation in order for recombinant strains of lactic acid bacteria to elicit mucosal IgA and/or serum IgG responses to the expressed antigen in a host.

Lactobacilli are Gram-positive, non-sporeforming rods. They are important members of the normal human oral, gastrointestinal, and genital flora and are non-pathogenic to humans and animals. *Lactobacillli* including *L. reuteri* have been found in the gastrointestinal tract of all mammals studied to this time (Mitsuoka, 1992) including humans, pigs, chickens, cattle, dogs, mice, rats and hamsters. The ubiquity of *Lactobacillus* species in the mammalian gastrointestinal tract combined with their ability to target and adhere to mucosal receptors make them useful organisms as vectors for vaccinating a host against a wide range of pathogens.

Although many infectious agents gain access to the body by colonizing mucosal surfaces, very few infections caused by these agents have been effectively prevented by using mucosal, i.e., oral immunization (Wells et al, "Lactic acid bacteria as vaccine delivery vehicles", *Antonie van Leeuwenhoek* 70:317, Kluwer Academic Publishers, 1996). Oral immunization is highly desirable because of ease and the low cost of vaccine delivery, storage and administration. An effective delivery vehicle or organism should be one that is normally present in the gastrointestinal tract of the host organism and must accurately target the mucosal sites of infection and adhere to the mucosal surface. *Lactobacilli* possess both of these characteristics. A useful vaccine delivery vehicle must, in addition, be capable of expressing antigens of interest at sufficiently high levels to successfully immunize the host and must be non-pathogenic to the host.

Previous work on oral vaccination has focused on the development of modified pathogenic bacteria as antigen delivery vehicles (Stocker, U.S. Patent No. 4,837,151, Auxotrophic Mutants of Several Strains of *Salmonella*; Clements et al., U.S. Patent No.

5,079,165, Avirulent Strains of *Salmonella*; Charles et al., U.S. Patent No. 5,547,664, Live-attenuated *Salmonella*). The efficacy of these bacteria as vaccines is thought to depend on their invasiveness, capacity to survive and multiply, and on adequate levels of antigen gene expression *in vivo*. It is unclear, however, whether pathogenic strains that are sufficiently attenuated to pose no danger to recipients will retain their ability to invade target areas, multiply, and express adequate antigen levels (Wells et al.). This has led the present inventors to investigate the use of lactic acid bacteria, *Lactobacilli* and particularly *L. reuteri*, that have been modified to express exogenous antigens.

Leer et al. (WO95/35389) disclose a method for introducing nucleic acid into microorganisms, including microorganisms such as *Lactobacillus* and *Bifidobacterium* species that are difficult to transform or transfect. The method of Leer et al. is based on limited autolysis before the transformation process is undertaken.

Published PCT application PCT/NL96/00409 describes methods for screening non-pathogenic bacteria, in particular lactic acid bacteria of the genera *Lactobacillus* and *Bifidobacterium*, for the ability to adhere to specific mucosal receptors. The method comprises screening for adherence factors found on these non-pathogenic bacteria that are structurally related to virulence factors of some pathogenic microorganisms. An expression vector is also disclosed that comprises an expression promoter sequence, a nucleic acid sequence, and sequences permitting ribosome recognition and translation capability. This reference indicates that various strains of *Lactobacillus* can be transformed so as to express heterologous gene products including proteins of pathogenic bacteria.

Oral administration of recombinant *L. lactis* has been used to elicit local IgA and/or serum IgG antibody responses to an expressed antigen (Wells et al.). This indicates that in *L. lactis*, expressed heterologous proteins may elicit antigenic responses in a host organism.

However, this reference and none of the prior art teaches that *L. reuteri*, a species with particularly desirable indigenous characteristics of mucosal targeting and adherence, can be transformed with heterologous DNA and express the foreign protein on the surface of the *L. reuteri* cell or secreted by the cell. The prior art fails to suggest or disclose the transformation of *Lactobacillus* with the aggregating gene *agg* or the mucin binding gene *muc* as set forth below.

U.S. Patent No. 5,413,960 to Dobrogosz teaches a method for obtaining the antibiotic ß-hydroxyproprionaldehyde, or reuterin, which is active against both Gram- positive and Gram-negative bacteria by culturing *L. reuteri* under anaerobic conditions in the presence of glycerol or glyceraldehyde. U.S. Patent No. 5,352,586 also to Dobrogosz describes a method of identifying strains of *L. reuteri* that produce the antibiotic reuterin. In both patents the antibiotic producing *L reuteri* strains are identified by their ability to inhibit the growth of susceptible microorganisms in the presence of glycerol or glyceraldehyde. These references provide a method for obtaining strains of *L. reuteri* that secrete the antibiotic reuterin useful in the treatment of infection caused by various pathogenic microorganisms.

U.S. Patent No. 5,439,678 claims a method for providing a probiotic to an animal which comprises feeding the animals *L. reuteri*. The term "probiotic" refers to ingested microorganisms that can live in a host and contribute positively to the host's health and well-being. The teachings of U.S. Patents 5,352,586, 5,439,678 and 5,413,960 are incorporated herein by reference. These patents, however, do not suggest or disclose the use of *L. reuteri* as a vaccine delivery vehicle.

Heng, N.C.K. et al. (Cloning and Expression of an Endo-1,3-1,4-β-Glucanase Gene from *Bacillus macerans* in *Lactobacillus reuteri*, *Appl. and Environ. Microbiol*, 3336-3340, Aug. 1997) describe the cloning, expression, and secretion of a heterologous gene derived

from another bacterial species in a strain of *L. reuteri* that originated in the gastrointestinal tract. The authors believe this to be the first demonstration of the expression of a gene of heterologous origin in *L. reuteri*. Heng et al. were also able to demonstrate secretion by *L. reuteri* of the gene product, β-glucanase, indicating that the heterologous secretion signals were recognized by the *L. reuteri* cells.

Summary of the Invention

In its broadest aspect, this invention discloses a method for vaccinating an animal by administering to said animal a recombinant *Lactobacilli* that have been transformed to express exogenous antigens. A particular example uses recombinant *L. reuteri* as the vaccine delivery vehicle which has been modified to express an epitope derived from enterotoxigenic *Escherichia coli (E. coli)* or enteropathogenic *E. coli*. One aspect of the invention relates to the discovery of genes responsible for the production of proteins that provide for the aggregation of individual cells and binding to mucin. The sequence for a gene (*agg*) that facilitates adhesion by controlling aggregation in *Lactobacillus* species is disclosed. The partial sequence for a gene (*muc*) that enhances binding to mucin is also disclosed.

Mucin is any of various mucoproteins that occur in the secretions of mucous membranes. The mucous membranes are rich in mucous glands which line an animal's body passages and cavities which communicate directly or indirectly with the exterior. Mucus is the viscid, slippery secretion that is usually rich in mucins and is produced by mucous membranes which it moistens and protects. Representative of the mucous membrane containing tissues which the vaccines of the present invention are effective in preventing or treating infections include the nasopharynx (nasal passages), pharynx, esophagus, stomach, small intestine and large intestine.

A method is provided for transforming *Lactobacilli* with the genetic information for an exogenous epitope derived from a pathogenic organism combined with additional copies of a *Lactobacillus agg* and/or *muc* gene and expressing the encoded proteins either on the cell surface or secreting the proteins from the cell. The recombinant *Lactobacilli* expressing *agg* and an exogenous antigen and/or *muc* and an exogenous antigen are then used as a vaccine to provide protection against disease caused by the donor pathogen. Examples of the method are provided using *L. reuteri*.

The invention further relates to recombinant *Lactobacillus* species that are capable of consistently and accurately reaching and adhering to target locations on the mucosa of the host and expressing there heterologous antigenic proteins derived from pathogenic organisms or from other biological material.

E. coli are Gram negative, non-sporeforming rods that are present in large numbers in the gastrointestinal tract of humans and animals. Some strains of *E. coli* cause gastroenteritis mediated by heat-labile and heat-stable enterotoxins comprising both endotoxins that are integral parts of the cell wall and exotoxins that are secreted by the bacterial cell. Secreted toxin is adsorbed to gangliosides at the brush border of epithelial cells of the small intestine. The genes for both types of toxins are located on plasmids. The plasmids carrying the genes for enterotoxins also carry genes that direct the synthesis of specific surface antigens that are essential for the attachment of *E. coli* to intestinal epithelial cells, such as one known as K88 isolated from piglet *E. coli*. Nucleic acid probes have been used to detect toxin genes. Maximum virulence is associated with specific adhesive fimbriae, hairlike projections on the bacterial cell surface. The primary function of fimbriae is to mediate adherence of the bacterial cell to other bacteria, to mammalian cells, or to hard and soft surfaces. This is an important feature in the pathogenesis of such microorganisms.

Both gastroenteritis produced by enterotoxigenic *E. coli* and childhood diarrhea caused by enteropathogenic strains of *E. coli* are mostly observed in underdeveloped countries. A safe and effective vaccine, would be extremely beneficial in preventing and treating disease caused by these organisms.

An additional aspect of the invention comprises the use of recombinant DNA technology to prepare expression vectors comprising genes encoding cellular aggregation (*agg*) and/or enhanced binding to mucin (*muc*) and DNA encoding an antigenic virulence factor obtained from a pathogenic microorganism, inserting the expression vectors into cells of a *Lactobacillus* species, and selecting transformed cells expressing the complete or partial heterologous protein at high levels. The invention further discloses the administration of such transformed *Lactobacillus* cells to an animal to provoke an immune response in the animal at a level and for a duration that will effectively vaccinate the animal against infection by the pathogenic microorganisms. The present invention optionally provides for the administration of antibiotics to the recipient mammal subsequent to administration of the transformed microorganism in order to eradicate the transformed microorganism from the vaccinated host.

Methods for preparing live vaccines from transformed strains of *Lactobacillus* species are also disclosed. The vaccines will be useful for vaccinating an animal host susceptible to disease from various pathogenic microorganisms, such as bacteria and viruses and also to create a desired immunological response to other biological materials. Transformed *Lactobacilli* serve as carriers for antigens so as to produce an immunologic response in the host. Transformed *Lactobacilli* can thereby serve as vaccine delivery systems to an animal in need of vaccination. The heterologous antigens expressed on the surface or secreted into the surroundings of the *Lactobacilli* will provide protection to the host.

A strain of *L. reuteri* is also provided which expresses an antigen of a pathogenic microorganism as a result of introducing into the *L. reuteri* cells an expression cassette comprising DNA sequences encoding the antigen under control of regulatory regions recognized by the *L. reuteri* cells.

There is further disclosed a method for vaccinating an animal with a live, non-virulent vaccine comprising the steps of: (a) identifying and selecting strains of non-pathogenic microorganisms such as *Lactobacilli* displaying desirable characteristics for targeting and adhering to mucosal tissue; (b) identifying and selecting those strains of non-pathogenic microorganisms such as *Lactobacilli* additionally demonstrating the potential to express foreign proteins; (c) identifying and isolating the gene or genes encoding antigenic proteins from a pathogenic microorganism or other biological material; (d) inserting the genes of step (c) into an appropriate expression cassette or construct containing regulatory regions recognized by a host microorganism identified in steps (a) and (b) and the genes *agg* and/or *muc*; (e) transferring the expression cassette into cells of the host microorganism to form a transformed organism; (f) selecting and growing the transformed cells that can express antigenic proteins encoded by the inserted gene sequences on their cell surface; and (g) combining the modified cells with pharmaceutically acceptable carriers and excipients to form a vaccine for oral, nasal or other direct delivery to mucosal surfaces. An additional step in the disclosed method is to use antibiotics to eradicate the transformed microorganisms after colonization.

Another aspect of the invention relates to the isolation, sequencing and expression of a gene, *agg*, identified in *Lactobacilli* that regulates the ability of the cells to aggregate *in situ*. Also disclosed is the isolation and partial sequencing of a gene, *muc*, and its expressed protein that increases the ability of a microorganism to adhere to the mucosa of an animal.

Detailed Description of the Invention

As used herein and in the claims, the term "animal" means mammals and avians, with humans being the animal of greatest interest. As used herein and in the claims, the term "*L. reuteri*" means any *Lactobacillus* microorganism that is identified as *L. reuteri* according to the method set forth in U.S. Patent 5,352,586. As used herein and in the claims, the terms "transformed *Lactobacilli* or "transformed *L. reuteri*" mean *Lactobacilli* or *L. reuteri* into which foreign genes encoding antigenic products have been inserted. Transformed *L. reuteri*, or other similarly transformed bacteria particularly other *Lactobacillus* species, may be administered in the form of a capsule, tablet, yogurt, solution or the like. Adequate dosages to establish transformed bacteria in the normal flora of an animal to effectuate vaccination is within the skill of the artisan. All embodiments of the invention require the use of viable transformed non-virulent bacteria, preferably *Lactobacilli* and more preferably *L. reuteri*, as the organism which provides for the production of antigenic products in the animal body at sites that elicit an immune response.

Vaccines according to the invention are prepared from live bacteria preferably *Lactobacilli*, and more preferably *L. reuteri*, that have been transformed so as to express antigens of microorganisms pathogenic to the host. The transformed bacteria, which serve as hosts for the expression of the antigen, can express the antigen in the cytoplasm which can then be translocated to the outer membrane of the microorganism or secreted to provide immunogens for an immunologic response by the animal host. By employing live, non-virulent bacteria as carriers for an immunogen, a strong targeted stimulus can be provided to the immune system. The antigen gene which is inserted into the host non-virulent bacteria

may come from diverse sources, such as pathogenic bacteria, viruses, fungi, protozoa, or other biological material.

The antigen gene may encode envelope proteins, capsid proteins, surface proteins or toxins such as exotoxins or enterotoxins. The antigen gene may also specify enzymes or other proteins needed for the synthesis of a polysaccharide or an oligosaccharide. The antigen genes are isolated in conventional ways employing probes where at least a partial amino acid or nucleic acid sequence is known. Representative of the antigen genes useful in transforming the *Lactobacilli* include those specifying the enterotoxins of enterotoxigenic or enteropathogenic *E. coli* or *Vibrio cholerae* strains; the HBsAg, surface, envelope or capsid proteins of *T. cruzi, B. pertussis, Streptococci, Haemophilus, Neisseria, Pseudomonas, Pasteurella, Chlamydia, Adenovrus, Astrovirus, herpes virus, myxovirus, retrovirus, rotavirus* and the like. The antigen gene may also specify an enzyme needed for synthesis of polysaccharides, e.g., *Meningococcus capsular* polysaccharide, or for the modification of an oligosaccharide or polysaccharide of the host microorganism. The preceding list is exemplary and not a comprehensive list of the possible sources of genetic information that may be transferred by the methods disclosed.

As an example, strains of *L. reuteri* that consistently and accurately target and adhere to mucosal surfaces, thereby demonstrating potential usefulness as a vehicle for the presentation of foreign antigens to the mucosa, are selected for transformation. Genes or DNA sequences encoding a heterologous antigen and, if desired, other genetic information are introduced into *L. reuteri* using molecular biology techniques known in the art.

Lactobacillus reuteri (*L. reuteri*), is a recently designated species of *Lactobacillus*. Some strains of this species were previously identified as *Lactobacillus fermentum*. *L. reuteri* is a symbiotic resident of the gastrointestinal tracts of humans, swine and other animals. The

neotype strain of *L. reuteri* is DSM20016 (ATCC No. 53609). This strain and other strains including *L. reuteri* 1063 (ATCC No. 53608) are available to the public at the American Type Culture Collection (Rockville, Maryland) having been deposited therein under the Budapest Treaty of April 17, 1987.

Some *Lactobacillus* species are known as recalcitrants as they are difficult to transform using known techniques. Various methods of transforming *L. reuteri* have been disclosed. One method for transforming *L. reuteri* is described in an International Application published under the Patent Cooperation Treaty, PCT 95/NL00215 (WO95/35389) to Leer et al. which is incorporated herein by reference. The method of Leer et al. requires subjecting *L. reuteri* to limited autolysis during or before the transformation process. Limited autolysis is carried out by incubating the microorganism in a low molarity electroporation buffer containing an osmotic stabilizer, generally at a pH of between 4 and 8 and at a temperature below 37°C, more preferably between 0 and 10°C.

A method for the construction of multi-purpose plasmid vectors and expression vectors for lactic acid bacteria is disclosed in PCT/NL95/9135 to Nederlandse Organisatie voor Toegpast Natuurwetenschappelijk Onderzoek (TNO). This method can be used to construct vectors that can be used for the introduction, stable maintenance, and efficient expression of foreign genes in lactic acid bacterial species including *Lactobacilli*. Modification of this method enables *Lactobacilli* to express, secrete, and display heterologous antigens on the cell surface and thereby function as an effective vaccine in its target location.

The expression vector disclosed in the instant application comprises an expression promoter sequence controlling a nucleic acid sequence encoding a heterologous antigenic protein or polypeptide or alternatively additional copies of a native *Lactobacillus* gene, such as *agg* or *muc*, whose expression it is desired to augment. The encoding nucleic acid sequence is

preceded by a 5' non-translated nucleic acid sequence comprising the minimal sequence required for ribosome recognition and RNA stabilization, followed by a translation initiation codon.

It is important that strains selected for transformation not only have the ability to express inserted genes encoding foreign protein they must also, in order to be effective as vaccine delivery vehicles, adhere efficiently to target mucous membranes. Therefore, *Lactobacilli* cells were selected that express adhesion factors efficiently.

The protocol for developing strains of *Lactobacilli*, in particular strains of *L. reuteri*, with improved adhesion factors comprises the following steps:

(1) isolating and characterizing genes involved in the synthesis and secretion of adhesion factors in *Lactobacilli*;

(2) selecting or constructing strains containing genes resulting in adhesion factors with improved properties; and

(3) demonstrating the capacity of strains with improved adhesion factors to displace and thereby interfere with adhesion of pathogenic bacteria to mucosal receptors.

The protocol for preparing a vaccine according to the present invention comprises the following steps:

(1) identifying and selecting strains of *Lactobacilli* displaying desirable characteristics for targeting and adhering to mucosal tissue efficiently;

(2) identifying and selecting strains of *Lactobacilli* additionally demonstrating the potential to express heterologous proteins;

(3) identifying and isolating the gene or genes encoding antigenic proteins of interest in a pathogenic microorganism or in other biological material;

(4) fusing the genes of step (3) with a gene *agg* encoding information for bacterial aggregation and/or a gene *muc* encoding information for bacterial binding to mucins;

(5) inserting the fused genes into an appropriate expression vector containing regulatory regions recognized by *Lactobacilli*;

(6) transferring the expression vector into the selected *Lactobacillus* cells;

(7) selecting and growing transformed *Lactobacillus* cells that can replicate and express antigenic determinants encoded by the inserted gene sequences on the cell surface;

(8) combining the transformed *Lactobacilli* with pharmaceutical carriers to form vaccine for oral, nasal or other direct delivery to mucosal tissue; and

(9) administering the vaccine to a human or other animal recipient.

EXAMPLE I

Enhancement of Aggregation

The ability to form multicellular aggregates has been reported for a number of bacterial species. This phenomenon is described either as autoaggregation, involving bacteria from the same strain, or as coaggregation where different bacterial strains are involved. Both types of aggregation have been described in *Lactobacillus* species. It has been suggested that autoaggregation and coaggregation are important for the ability of the bacteria to colonize and thereby effect the removal of intestinal pathogens. In *Lactobacilli*, there is a demonstrated connection between aggregation and genetic exchange. It has been reported that a 32 kD aggregation promotion factor in *L. plantarum* is immunologically crossreactive with a protein of similar size that mediates aggregation in *Lactobacilli*.

This experiment is directed to a cloned and sequenced gene from *L. reuteri* that encodes a 60 kD protein that mediates aggregation. Introduction of additional copies of the

gene into an *L. reuteri* strain markedly enhanced aggregation behavior. The sequenced gene was found to have extensive sequence homology to a large family of ATP-dependent RNA helicases. It was demonstrated in this work and disclosed herein that autoaggregation by *L. reuteri* involves the activity of a protein with extensive homology to RNA helicases.

Materials and Methods

<u>Bacterial Strains and Growth Conditions</u>

In this experiment, a strain of *Lactobacilli* known as *L. reuteri* 1063 was used to isolate the gene for a 60 kD protein which demonstrates aggregating activity *in vitro* and *in vivo*. *L reuteri* strains 1063 and 1068 were previously isolated from the small intestine of a pig. *L. reuteri* DSM 20016 was obtained from the "Deutsche Sammlung von Mikroorganismen", Göttingen, Germany. *E. coli* LE392 was used as lambda (λ) host strain and *E. coli* TG1 as host strain in subcloning and expression of the recombinant protein. *L.reuteri* were grown on Man-Rogosa-Sharpe (MRS) agar or in MRS broth (Oxoid Ltd., Basingstoke, England). Plates were incubated in anaerobic jars under CO_2 and N_2 atmosphere (GasPak System, BBL, Cockeysville, MD, USA) at 37°C. *E. coli* broth cultures were grown at 37°C in Luria-Bertani (LB) broth on a rotary shaker or on LB agar. When antibiotics were used for selection, the concentrations were: 50 µg/ml Ampicillin (Amp) and 8 µg/ml Chloramphenicol (Cm) for both *E. coli* and *Lactobacilli.*

Proteins and Reagents

L. reuteri strain 1063 was grown in 500 ml MRS broth and the cells were harvested by centrifugation at 10,000 x g. The spent culture medium was dialysed and subsequently lyophilized. The bacteria were washed repeatedly with 500 ml portions of distilled water until the autoaggregating activity was lost. The wash solutions were also dialysed and lyophilized. Antiserum against a mix of the high molecular weight (MW) fractions from the spent growth medium and the wash solutions were raised in a rabbit. The rabbit was immunized with the proteins and given three booster doses in two week intervals. The animal was sacrificed eight weeks after the first immunization.

In order to make the antiserum more specific against the aggregation factor. it was adsorbed against the nonaggregating *L. reuteri* strain 1068. The bacteria were grown in 200 ml MRS for 16 hours and washed twice in phosphate-buffered saline (PBS) at pH 7.3 supplemented with 0.05% Tween 20 (PBST). The cells were then suspended in 20 ml PBST. One ml of antiserum was mixed with 1 ml of bacterial suspension and incubated at room temperature for two hours. After centrifugation the adsorbed antiserum were sterile filtered through a 0.2 μm filter. The IgG-fraction from the adsorbed antiserum was purified on ProteinA-Sepharose (Pharmacia, Uppsala, Sweden) according to the manufacturer's instructions.

Construction and Screening of a λ-Library

L.reuteri strain 1063 was grown in 100 ml MRS broth and DNA was extracted according to Axelsson and Lindgren (1987). The DNA was partially digested with *Sau*3A and ligated into Lambda EMBL3 *Bam*HI arms. Packaging into phage particles was performed according to the manufacturer's instructions (Promega, Madison, WI, USA). After

infection of *E. coli* LE392. the resulting plaques were screened with the IgG-fraction from the antiserum (Roos et al., *FEMS*, Microbiology Letters, 144:33-38,1996).

Affinity Purification of Recombinant Protein

The IgG-fraction of the antiserum was coupled to CnBr-activated Sepharose (Pharmacia) according to the manufacturer's instructions. Positive λ-clones from the screening procedure were used to produce large scale λ-lysates (Maniatis et al., *Molecular Cloning, A Laboratory Manual*, 1982). The lysates were centrifuged and applied to the Sepharose coupled with the Ig-G fraction. The column was washed with PBS until A_{280} of the collected fractions had reached the baseline. The adsorbed proteins were eluted with 1 M HAc. After neutralization with 1 M Tris-Base the eluted proteins were dialysed twice against a large volume of distilled water. The protein material was then lyophilized and dissolved in PBS.

Aggregation Assay

The affinity purified protein from the different classes of recombinants was examined for the ability to aggregate *L. reuteri in vitro*. *L.reuteri* 1063 was grown in 10 ml MRS for sixteen hours. The bacteria were washed five times with 10 ml of distilled water which resulted in a loss of aggregation. The bacteria were suspended in 1 ml of distilled water and 10 μl of bacterial suspension was mixed with 1 μl of affinity purified protein on a microscopy slide glass. Occurrence of aggregates within one minute was recorded as a positive test.

Subcloning and Isolation of Positive Clones

DNA from λ-clone 105:2 was isolated and cleaved in separate reactions with *Eco*RI, *Hind*III, *Pst*I, *Sal*I and *Sca*I. The material from the different cleavages were pooled, treated with T4 DNA polymerase in order to generate blunt ends, and then ligated into a *Sma*I cleaved pUC18 vector. The ligation mix was electroporated into *E. coli* TG1 cells and the

resulting clones were selected on LA plates supplemented with Amp and screened with the IgG-fraction from the antiserum. Plasmids from positive clones were purified with Wizard Minipreps DNA purification system (Promega) and characterized with restriction enzyme analyses and sequencing.

Introduction of the *Agg* Gene into *L.reuteri* Strains

A broad host range vector, pVS2, (von Wright et al., *Applied Environ. Microbiol* 53:1584-1588, 1987) harboring a chloramphenicol resistance gene was cleaved with *Hind*III and blunt ends were generated by treatment with T4 DNA polymerase. A 2450 bp *Bgl*II fragment of chromosomal DNA was also treated with T4 DNA polymerase and thereafter ligated at the single *Cla*1 site into pVS2. This construct is called pAGG1. The ligation mix was electroporated into *E. coli* TG1 cells and transformants were selected on plates with chloramphenicol (Cm) and screened with the IgG-fraction. The plasmid from one positive clone was electroporated into *L. reuteri* DSM 20016 and strain 1068 according to the method of Ahrné et al., (*Current Microbiology* 24: 199-205), and transformants were selected on MRS plates with chloramphenicol. In order to detect an *in vivo* effect of the gene, the resulting clones were grown in 10 ml MRS supplemented with Cm for 16 hours at 37°C.

DNA Sequencing and Analysis of the Sequence

Sequencing was performed by the dideoxy method, using ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer, Foster City, CA, USA) with commercial standard and customized sequencing primers. The sequencing samples were analyzed on the automatic sequencing machine ABI 373 (Perkin-Elmer). The PC/GENE DNA and protein data handling package was used for analysis of the DNA and deduced protein sequence.

SDS-PAGE and Western Blotting

SDS-PAGE and Western blot analyses were performed with the PhastSystem (Pharmacia) according to the manufacturer's instructions and the proteins were blotted to a Protran BA85 nitrocellulose membrane (Schleicher and Schüell, Dassel, Germany) by diffusion at 65°C for 45 minutes. Blocking of the membranes, incubations with the IgG-fraction and HRP-conjugated secondary antibody was performed according to Roos et al., 1996. The membranes were finally developed with 4-chloro-1-naphtol as substrate.

Results

The *agg* gene of *L.reuteri* strain 1063 was cloned and found to reside on a 2450 bp chromosomal *Bgl*II fragment. As described above, antiserum was raised against extracellular and cell surface proteins from *L.reuteri* strain 1063 and was used to screen a λ-library generated from the same strain. A large number of clones were identified that were reactive with the antiserum. Further examination of the recombinant proteins expressed by these clones showed that they represented three different classes as judged by band pattern in Western blot analyses. Representatives from the different classes of clones were used to produce recombinant protein which was subsequently affinity purified on the immobilized IgG-fraction of the same antisera that was used in the initial screening. One class of clones expressed a 60 kD protein that promoted aggregation in a glass slide experiment. Subcloning of the DNA from one of these clones, λ105:2, into a plasmid vector allowed identification of clones reacting with the antisera and expressing a protein band of the same size as the λ-clone. One of these clones, designated LrAg7, was harboring a 3.4 kb *Hind*III fragment. Further deletions and subclonings allowed the identification of a 2450 bp chromosomal *Bgl*II fragment encoding the responsible protein.

Sequence analysis of the *Bgl*II fragment revealed an open reading frame of 1491 nucleotides (nt) coding for a polypeptide containing 497 amino acids with a predicted

molecular mass of 56 kD. The initiation codon TTG is preceded by a ribosome binding site, and further upstream, by possible transcription initiation signals. The deduced amino acid sequence was used for homology searches in the data banks and extensive sequence similarity to the large family of DEAD-box helicases was found. The best match was with a *Bacillus subtilis* protein that is a proposed ATP-dependent RNA helicase. Nucleotide and amino acid sequences for the *agg* gene are provided as directed in 37 C.F.R .§1.821 through §1.825 and are identified as SEQ ID No:1 in the Sequence Listing.

In order to establish that the *agg* gene is actually encoding a protein with aggregating effect *in vivo*, the *Bgl*II fragment was cloned into the broad host range vector pVS2 and the construct was introduced into *L.reuteri*. The gene was introduced into *L.reuteri* 1063, which has an aggregating phenotype. The transformed microorganisms exhibited markedly enhanced aggregation compared with the native microorganism.

EXAMPLE II

Use Of The *Agg* Gene In A Gene Fusion System For Expression And Secretion Of Fused Proteins

Using recombinant DNA techniques, as described in Example I, expression vectors containing heterologous genes of interest are prepared and inserted into *Lactobacillus* cells that have demonstrated capability for expressing a protein encoded by inserted genes.

Fusion of the *agg* gene to the gene for K88ab fimbriae:

The *agg* gene of *L.reuteri* strain 1063 was cloned and defined to reside on a 2450 bp chromosomal *Bgl*II fragment as described in Example I. This *Bgl*II fragment of chromosomal DNA was cloned at the single *Cla*I site of the plasmid vector pVS2 (von Wright et al., 1987). Before ligation the chromosomal fragment and the vector were treated with T4 DNA

polymerase to create blunt ends (Maniatis et al., 1982). This construct, pAGG1, was cleaved at position 1622 with *Cla*1 to generate a linear molecule.

The gene encoding the K88ab fimbriae of *E. coli* was identified by Gaastra, W. et al., (The nucleotide sequence of the gene encoding the K88ab protein subunit of porcine entertoxic *Escherichia coli*. *FEMS Microbiol. Lett.* 12: 41-46, 1981); and characterized by Bakker et al., (Characterization of the antigenic and adhesive properties of FaeG, the major subunit of K88 fimbriae. *Mol. Microbiol.* 6 (2): 247-255, 1992). PCR was used to identify a suitably useful fragment of the K88ab gene. PCR primers used were as follows:

5'-AAATCGATGCCTGGATGACTGGTGAT-3'; and

5'-AAATCGATTAGGCAGCAGAAACAACAGT-3'.

Standard PCR procedures (Ehrlich, H. A. and Arnheim, N., *Annu Rev. Genet.* 26: 479-506, 1992) are followed to obtain a 705 bp product. The product of PCR is cleaved with *Cla*I and ligated into *Cla*I cleaved pAGG1. The resulting construct is electrotransformed into *E. coli* TG1 cells and the resulting transformants analyzed to identify clones containing the fused genes. An identified clone is verified by sequencing and denoted as pKAGG1.

Introduction of the fusion gene construct pKAGG1 into *L.reuteri*

The construct pKAGG1, expressing a fusion protein consisting of part of the AGG protein from *L.reuteri* and part of the K88ab fimbriae of *E. coli* is electrotransformed into *L.reuteri* strains 1063 and 1068 using the method of Ahrne et al., (Ahrne, S., Molin, G., and Axelsson, L. Transformation of *Lactobacillus reuteri* with electroporation: Studies on the erythromycin resistance plasmid pLUL631. *Current Microbiol.* Vol 24, 199-205, 1992). Transformants are isolated on agar plates containing 10 mcg/ml erythromycin. The production of fusion protein is detected by using antibodies against either the AGG protein and/or antibodies against the K88ab fimbriae.

Using the methodology of the present invention genes encoding enterotoxins secreted by enterotoxigenic or enteropathogenic strains of *E. coli* are fused to the *agg* gene of *L.reuteri* and inserted into an expression cassette having an appropriate promoter sequence and other regulatory regions recognized by *L.reuteri* cells. The cassette is then transferred into *L.reuteri* cells that have been determined to be capable of expressing inserted genes. Cells that have been successfully transformed and express the inserted genes, as indicated by the presence of *E. coli* antigens on the cell surface are selected for immunologic evaluation. *L.reuteri* cells expressing *E. coli* antigens are placed in a suitable pharmaceutical carrier or food product such as milk or yogurt and delivered as a vaccine to mammals susceptible to infection by toxic strains of *E. coli*. Vaccinated and unvaccinated mammals are challenged with live enterotoxigenic *E. Coli* (ETEC) and evaluated for subsequent infection in order to determine whether the antigen expressing *Lactobacilli* conferred protective immunity.

The described procedure can be used with a wide variety of pathogenic organisms for which genes for antigenic factors are available by transferring appropriate genes into competent *L. reuteri* or other *Lactobacilli* that have either the *agg* gene or a homologous

gene. *Lactobacilli*, particularly *L. reuteri*, are the preferred hosts for the plasmid containing the fused genes, however, the procedure can be used to transform other bacterial species. The procedure can also be modified so that the fused genes can be inserted directly into the host chromosome instead of being introduced on a plasmid vector.

EXAMPLE III

Use Of The *Agg* Gene In A Gene Fusion System That Is Integrated Into The Chromosome Of A Recipient Cell

Using recombinant DNA techniques described in Examples I and II, expression vectors containing heterologous genes of interest and prepared, inserted into *L. reuteri* cells and integrated into the chromosome of the cell.

The *agg* gene and the K88 gene of *E. coli* described in Examples I and II were cloned into a temperature sensitive shuttle vector, pJRS233, whose construction is described in Perez-Casal et al. (*Molec. Microbiol.* 8(5):809-819, 1993). The vector pJRS233 was generated from a temperature sensitive plasmid demonstrated by Maguin et al. (New Thermosensitive Plasmid for Gram-Positive Bacteria, *J. Bacteriol.* 174:5633-5638, 1992) to be stable at temperatures below 35°C in lactic acid bacteria. The *Cla* I site in pJRS233 was initially cleaved with *Cla*I, thereby destroying the site, then treated with T4 polymerase, and religated. The *Bgl*II fragment with the *agg* gene, described in Example I, was cloned into the *Bam*HI site of modified pJRS233 and the PCR fragment from the K88 gene, described in Example II, was cloned into the *Cla*I site. The resulting construct containing both the *agg* and K88 genes is called pAGGts1.

Plasmid pAGGts1 was electrotransformed into *L. reuteri* 1063. Integration of the plasmid into the chromosome of *L reuteri* was accomplished by a modification of the method of Bhowmik et al. (*J. Bact.*, pp. 6341-6344, Oct. 1993). The construct pAGGts1 is a

temperature sensitive integration plasmid that can be introduced and propagated in *Lactobacillus* species, including *L. reuteri*. After introduction of the plasmid, the bacteria were propagated at 46°C, a non-permissive temperature, in order to turn off replication of the plasmid and select for clones in which the construct had been inserted into the chromosome. Clones in which the native gene and the vector have been deleted were isolated as described in Bhowmik et al.

EXAMPLE IV

Identification Of A Gene, *Muc*, And Its Protein That Enhances Binding To Mucins

In order to further identify strains of *Lactobacilli* with strong adhesive properties, work was done to identify a gene and its expressed protein that would enhance binding to intestinal cell surface proteins called mucins. Found and disclosed herein is a protein greater than 200 kD that enhances binding of *L.reuteri* to mucin. Subcloning and sequencing identified the *muc* gene.

Materials and Methods

In this experiment, the 1063 strain of *L. reuteri* was used to isolate the 200 kD proteins that provide for binding to mucins. The bacterial strains, growth conditions, reagents, construction and screening of the λ-library, and the affinity purification of the recombinant protein was as set forth in Example I. The mucin binding protein was isolated from the culture media as described herein.

Western Blotting: Conducted as described in Example I. Primary antibody (p108) against the mucus binding protein was purified from a rabbit injected with the original solution of culture medium and water wash from strain 1063.

Mucin binding assay: Partly purified mucin from porcine stomach obtained from Sigma (St. Louis, Mo.)was suspended in a carbonate buffer at pH 9.7 at a concentration of 0.1 mg/ml. 200 µl of the solution was pipetted into microtiter wells and were left for coating at 37°C for approximately 3 hours. The wells were blocked by the addition of 200 µl of PBS 1% Tween20 at room temperature for 1 hour and then washed 3 times with PBST 0.5%Tween 20 (PBST). Bacteria were grown in MRS broth overnight at 37°C, then washed and resuspended in PBST. Optical density (OD) of the bacterial cells was measured at 600 nm in a Beckman DU650 spectrophotometer and adjusted to OD 0.5. 150 µl of the bacterial suspension was loaded into triplicate wells and incubated at 37°C for approximately 2 hours. Wells were washed 3 times and 200 µl/well of 1% SDS, 0.2 MNaOH was added and incubated for 15 minutes at room temperature. After gently mixing, 50 µl was taken in order to measure the amount of bound bacteria.

Inhibition Assay: The affinity purified proteins from the different λ-clones were tested in the mucin binding assay. Prior to the addition of the bacteria to the wells, 10 µl of a solution of the purified protein with A_{280}=0.1 was added. The proteins were incubated for 30 minutes in the wells before the bacteria were added, without any washing of the well. The amount of bound bacteria were compared with a sample without addition of protein and also with a sample with addition of an equal amount of ovalbumin (Sigma). All samples were analyzed in triplicate.

Subcloning: DNA from λ-clone 1208:21 was isolated, subcloned and positive clones were isolated as described in Example I.

DNA Sequencing and Analysis of the Sequence

Sequencing was performed by the dideoxy method, using ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer, Foster City, CA, USA)

with commercial standard and customized sequencing primers. The sequencing samples were analyzed on the automatic sequencing machine ABI 373 (Perkin-Elmer). The PC/GENE DNA and protein data handling package was used for analysis of the DNA and deduced protein sequence.

SDS-PAGE was conducted as set forth in Example I.

Results

Southern blotting: The *muc* gene was found to be present in *L.reuteri* strain 1063.

Western blotting: Mucin binding protein was observed only in the culture medium and not in the water wash.

The *muc* gene of *L. reuteri* strain 1063 was cloned and found to reside on a 6.2 kb *Eco*RI fragment. As described in Example I, different classes of clones were found when screening the λ-library with the antiserum. One class of clones expressed a <200kDa protein that promoted adhesion of the bacteria to mucin. Subcloning of the DNA from one of these clones, λ108:21, into a plasmid vector allowed identification of clones reacting with the antisera and expressing a protein band of the same size as the λ-clone. One of these clones designated LrMu3 was harboring a 6.2 kb *Eco*RI fragment. Sequence analysis of the *Eco*RI fragment reveal an open reading frame preceded by a ribosome binding site and the possible transcription initiation signals. The nucleotide and amino acid sequences for the *muc* gene have been partially determined. They have been assigned the identifier Seq ID No: 2 in the Sequence Listing. Recombinant forms of strains that express a gene that promotes cellular aggregation, *agg*, and a gene mediating adherence to mucin, *muc*, as well as expressing foreign antigens on the cell surface are shown to be useful to vaccinate and thus protect the host against infection by the pathogenic microorganisms whose gene or genes have been inserted.

Industrial Applicability

While the health benefits of vaccination against gastrointestinal pathogens are clear, finding safe and effective vaccines presents challenging problems. The disclosed discovery provides a method for vaccination of an animal with a microorganism containing genes that are responsible for the production of proteins that provide for the aggregation of individual cells and/or binding to mucosa cells and/or mucous and can be transformed so as to express foreign antigens.

The method of the invention described and claimed herein can be used in the pharmaceutical and food industries to prepare vaccines against pathogenic microorganisms or other biological material. The vaccine can be ingested by an animal in a pharmaceutically acceptable carrier or it can be added to milk or milk products such as yogurt. The vaccine can also be administered nasally or through other direct administration to mucosal tissues and/or mucous. Vaccination of an animal, with transformed *Lactobacilli*, preferably *L. reuteri*, as described herein serves to prevent or treat diseases immunologically associated with the host's mucosa.

While certain representative embodiments have been set forth herein, those skilled in the art will readily appreciate that modifications can be made without departing from the spirit or scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Casas, Ivan
Jonsson, Hans
Möllstam, Bo
Roos, Stefan

(ii) TITLE OF INVENTION: Lactobacilli Harboring Aggregation and Mucin Binding Genes As Vaccine Delivery Vehicles

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Dublin

(D) STATE: Ohio

(E) COUNTRY: US

(F) ZIP: 43017

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44Mb storage

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: MS-DOS Version 6.22

(D) SOFTWARE: Microsoft Word Version 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/039,773

(B) FILING DATE: 16-MAR-1998

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA: Not applicable

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 29,092

(C) REFERENCE/DOCKET NUMBER: 1229-005

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(B) TELEFAX: (614) 792-5536

(C) TELEX: Not applicable

(2) INFORMATION FOR SEQUENCE ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Genomic DNA

(A) DESCRIPTION: Genomic DNA sequence and deduced amino acid sequence of bacterial aggregation protein

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus reuteri* sp

(B) STRAIN: 1063

(C) CELL TYPE: Unicellular organism

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1

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ATTAATTGCC GATCTTACGG CTACTTTGAC AGGTGAGGAT ATTGTTCTAT      50

TGAAAGCAAG CCATGGTATT CACCTAGAAG AAGTCTTGAC GGCATTAAAA     100

GCAGAATAGT TAATATATTT GCCAGTCGAT TACTGATGCT TATATCATGA     150

ATCGACTGGT CATTTTTAGG AGGAAAATTT TTG AAG TTT AGT GAA TTA   198
                                 Met Lys Phe Ser Glu Leu
                                  1               5

GGC TTA TCC GAT AGC CTA TTA AAA GCA ATC AAA CGG AGC GGA    240
Gly Leu Ser Asp Ser Leu Leu Lys Ala Ile Lys Arg Ser Gly
            10                  15                  20

TAC GAA GAA GCA ACA CCA ATT CAA GAA CAA ACG ATT CCA ATG    282
Tyr Glu Glu Ala Thr Pro Ile Gln Glu Gln Thr Ile Pro Met
                25                  30

GTT CTT GAG GGT AAG GAT GTT ATT GGT CAA GCA CAG ACT GGA    324
Val Leu Glu Gly Lys Asp Val Ile Gly Gln Ala Gln Thr Gly
 35                  40                  45

ACT GGT AAG ACG GCT GCT TTT GGG TTG CCA ATT ATT GAA AAC    366
Thr Gly Lys Thr Ala Ala Phe Gly Leu Pro Ile Ile Glu Asn
     50                  55                  60

GTT GAT ACT GAA AAT CCC AAT ATT CAA GCA ATT ATC ATT TCA    408
Val Asp Thr Glu Asn Pro Asn Ile Gln Ala Ile Ile Ile Ser
         65                  70                  75

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            80                  85                  90

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Arg Leu Gly Lys Asp Lys His Val Arg Val Gln Val Val Tyr
                95                 100

GGT GGG GCA GAT ATT CGG CGC CAA ATT AAG AGC TTG AAA CAA    534
Gly Gly Ala Asp Ile Arg Agr Gln Ile Lys Ser Leu Lys Gln
105                 110                 115

CAC CCC CAA ATT CTC GTG GGG ACC CCT GGA CGG TTA CGT GAC    576
His Pro Gln Ile Leu Val Gly Thr Pro Gly Arg Leu Arg Asp
    120                 125                 130
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CAT ATT AAC CGT CAT ACA GTT AAA CTT GAC CAC ATT AAG ACC      618
His Ile Asn Arg His Thr Val Lys Leu Asp His Ile Lys Thr
        135                 140                 145

CTG GTT CTC GAT GAA GCA GAT GAA ATG CTA AAC ATG GGA TTC      660
Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe
            150                 155                 160

TTA GAA GAT ATT GAA TCC ATC ATC AAG GAA ACA CCA GAT GAT      702
Leu Glu Asp Ile Glu Ser Ile Ile Lys Glu Thr Pro Asp Asp
                165                 170

CGG CAA ACT TTG CTC TTC TCA GCA ACC ATG CCA CCA GAA ATC      744
Arg Gln Thr Leu Leu Phe Ser Ala Thr Met Pro Pro Glu Ile
175                 180                 185

AAG CGA ATT GGG GTT CAA TTT ATG TCT GAT CCG GAA ACT GTG      786
Lys Arg Ile Gly Val Gln Phe Met Ser Asp Pro Glu Thr Val
    190                 195                 200

CGG ATC AAG GCC AAG GAA TTG ACT ACT GAC TTA GTT GAT CAG      828
Arg Ile Lys Ala Lys Glu Leu Thr Thr Asp Leu Val Asp Gln
        205                 210                 215

TAC TAT GTT CGC GCT CGT GAC TAT GAA AAG TTT GAC ATC ATG      870
Tyr Tyr Val Arg Ala Arg Asp Tyr Glu Lys Phe Asp Ile Met
            220                 225                 230

ACC CGC TTA ATT GAT GTT CAA GAT CCT GAC TTA ACA ATT GTC      912
Thr Arg Leu Ile Asp Val Gln Asp Pro Asp Leu Thr Ile Val
                235                 240

TTT GGT CGG ACA AAG CGG CGG GTA GAT GAA TTG TCG AAG GGC      954
Phe Gly Arg Thr Lys Arg Arg Val Asp Glu Leu Ser Lys Gly
245                 250                 255

TTG ATT GCG CGT GGC TAC AAT GCA GCT GGT ATC CAT GGT GAC      996
Leu Ile Ala Arg Gly Tyr Asn Ala Ala Gly Ile His Gly Asp
    260                 265                 270

CTT ACT CAG GAT AAG CGT TCT AAG ATC ATG TGG AAG TTT AAG     1038
Leu Thr Gln Asp Lys Arg Ser Lys Ile Met Trp Lys Phe Lys
        275                 280                 285

AAC AAT GAA CTT GAT ATC TTA GTT GCA ACA GAT GTG GCT GCC     1080
Asn Asn Gly Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala
            290                 295                 300
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CGG GGC TTA GAC ATT TCG GGG GTT ACG CAT GTT TAT AAT TAT 1122
Arg Gly Leu Asp Ile Ser Gly Val Thr His Val Tyr Asn Tyr
305 310

GAT ATT CCA TCT GAC CCA GAC AGC TAT GTT CAC CGG ATT GGC 1164
Asp Ile Pro Ser Asp Pro Asp Ser Tyr Val His Arg Ile Gly
315 320 325

CGA ACA GGA CGG GCC GGA CAT CAC GGG GTA TCT TTA ACC TTT 1206
Arg Thr Gly Arg Ala Gly His His Gly Val Ser Leu Thr Phe
330 335 340

GTG ACT CCA AAT GAG ATG GAT TAC CTT CAT GAG ATT GAA AAA 1248
Val Thr Pro Asn Glu Met Asp Tyr Leu His Glu Ile Gly Lys
345 350 355

TTA ACC CGG GTA CGG ATG TTG CCA CTC AAG CCA CCA ACA GCT 1290
Leu Thr Arg Val Arg Met Leu Pro Leu Lys Pro Pro Thr Ala
360 365 370

GAA GAA GCA TTT AAG GGT CAA GTA GCA TCG GCC TTT AAT GAT 1332
Glu Glu Ala Phe Lys Gly Gln Val Ala Ser Ala Phe Asn Asp
375 380

ATC GAT GAA TTA ATC GCG CAG GAT TCA ACT GAT CGT TAT GAA 1374
Ile Asp Glu Leu Ile Ala Gln Asp Ser Thr Asp Arg Tyr Glu
385 390 395

GAA GCC GCT GAA AAG CTA TTA GAA ACT CAT AAT GCA ACT GAC 1416
Glu Ala Ala Glu Lys Leu Leu Glu Thr His Asn Ala Thr Asp
400 405 410

CTA GTA GCA GCA TTG TTA AAT AAC ATG ACG AAG GAA GCA GCG 1458
Leu Val Ala Ala Leu Leu Asn Ans Met Thr Lys Glu Ala Ala
415 420 425

AGT GAG GTT CCC GTT AAG ATT ACC CCT GAG CGT CCC CTT CCA 1500
Ser Glu Val Pro Val Lys Ile Thr Pro Glu Arg Pro Leu Pro
430 435 440

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CGG CGT AAT AAG CGG AAT AAC CGT AAT GGC AAC CGC AAT AAC      1542
Arg Arg Asn Lys Arg Asn Asn Arg Asn Gly Asn Arg Asn Asn
                445                     450

TCG CAT GGT GGC AAC CAC TAC CGG CGT AAG AAT TTC CGT CGT      1584
Ser His Gly Gly Asn His Tyr Arg Arg Lys Asn Phe Arg Arg
455                 460                     465

CAC CAA CAT GGC AGT CAT CGA AAT GAT AAC CAT GGG AAG AGC      1626
His Gln His Gly Ser His Arg Asn Asp Asp His Gly Lys Ser
    470                 475                     480

CAT TCC AGT CGT CAT TCA TTT AAT ATT CGG CAC CGG AAA GAA      1668
His Ser Ser Arg His Ser Phe Asn Ile Arg His Arg Lys Gly
        485                 490                     495

AAT TAA TTA TGA AGCCTTTGGT TGTGACGTGT ACCCTTAAAG             1710
Asn

TTGGAACTTG TATGTTCTTA CTTGTAAATT GAATAATTAT                  1750

TTTTCTTAGG CAACTAAATT CTGCTCGTAT TGGAGTGGTG TTTGGTTGCC       1800
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(2) INFORMATION FOR SEQUENCE ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2601 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Genomic DNA

(A) DESCRIPTION: Partial genomic DNA sequence and deduced amino acid sequence of mucin binding protein

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus reuteri* sp

(B) STRAIN: 1063

(C) CELL TYPE: Unicelluar organism

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2

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TTCTTAGTGA TTTTCCAGAA GTTCAGGATT TTCAGGAAAA GTAAAAAAGA     200

GACTGAGGAG ATTATTTCCT AGTCTCTATC TTTTTAAAGT AGGGTAATAA     250

CCTTGTTTTC ACTTTCGTTA TTTCCCGGGA AATAGAAAGA AGCGCTAAAA     300

ATG AGA AAG ATT GGA ATT GTT GGC CTC GGT CAT GTG GGT GAA    342
Met Arg Lys Ile Gly Ile Val Gly Leu Gly His Val Gly Glu
 1              5                   10

ATG CTA GCC AAC CAA TTA GTA ATG AAC GGA AAA GTT GAT GAA    384
Met Leu Ala Asn Gln Leu Val Met Asn Gly Lys Val Asp Glu
 15                 20                  25

TTA GTT TTG ATT GAT GAA AAA GAT CCA CAA AAA GGT CAA AAG    426
Leu Val Leu Ile Asp Glu Lys Asp Pro Gln Lys Gly Gln Lys
     30                 35                  40

ACG GTT ACA CAG ACA ATT AAG TAC GAA TAC GCT GAT GGC ACG    468
Thr Val Thr Gln Thr Ile Lys Tyr Glu Tyr Ala Asp Gly Thr
        45                  50                  55

GCA ACT GGT TTG GCT GAT AAT GTG CAA ACC TTG ACG TTC AAG    510
Ala Thr Gly Leu Ala Asp Asn Val Gln Thr Leu Thr Phe Lys
            60                  65                  70

CGT ACA GGT GAC AAG GAT CTC GTT ACT CAT GAA GTA ACC TGG    552
Arg Thr Gly Asp Lys Asp Leu Val Thr His Glu Val Thr Trp
                75                  80
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CCA GAC TGG TCA ACG GTT GCC GGT CAA CAA ACC AGT GTT GTA      594
Pro Asp Trp Ser Thr Val Ala Gly Gln Gln Thr Ser Val Val
 85                  90                  95

ACC AGT CCA GCT CTC AAG GGC TAC ACT GCT GAT ACC AAC GAA      636
Thr Ser Pro Ala Leu Lys Gly Tyr Thr Ala Asp Thr Asn Glu
    100                 105                 110

ATT CCA GCC ATT ACC TAC CAT GCT GGT GAC AGT GAT GTT ACT      678
Ile Pro Ala Ile Thr Tyr His Ala Gly Asp Ser Asp Val Thr
        115                 120                 125

TAT GTT GTT AAG TAC AAT GCC GAT GTT CAA CAT GCT GTT ATC      720
Tyr Val Val Lys Tyr Asn Ala Asp Val Gln His Ala Val Ile
            130                 135                 140

AAT TAC ATT GAT GGC GAA AGT GAT GAG ATA CTG CAC ACT GAT      762
Asn Tyr Ile Asp Gly Glu Ser Asp Glu Ile Leu His Thr Asp
                145                 150

AAG GTT AAT GGC CAC TCT GAC GAA AAG ATC AAC TAC AGC ACT      804
Lys Val Asn Gly His Ser Asp Glu Lys Ile Asn Tyr Ser Thr
155                 160                 165

GCT GAT ATG ATC AAA CAG TTG GAA GCC AAG GGT TAT GAA CTG      846
Ala Asp Met Ile Lys Gln Leu Glu Ala Lys Gly Tyr Glu Leu
    170                 175                 180

TTC AAG GAC AAC TTC CCA GCT GGT GAG AAG TTC GAT AAC GAT      888
Phe Lys Asp Asn Phe Pro Ala Gly Glu Lys Phe Asp Asn Asp
        185                 190                 195

GAC ACC AAC GAT CAA TTC TAC ACG GTA ATC TTC AAG CAC CAT      930
Asp Thr Asn Asp Gln Phe Tyr Thr Val Ile Phe Lys His His
            200                 205                 210

CGT GAA AAC GTT GAT CCA AAC CAC TCC TCG GCT GAT GGC ACG      972
Arg Glu Asn Val Asp Pro Asn His Ser Ser Ala Asp Gly Thr
                215                 220

AAG GGT ACG AAG ACG CTG ACG GAA ACG GTT CAC TAC AAG TAC      1014
Lys Gly Thr Lys Thr Leu Thr Glu Thr Val His Tyr Lys Tyr
225                 230                 235

GCT AAT GGC ACC AAG GCG GCT GAA GAT CAG ACG GCT CAG GTA      1056
Ala Asn Gly Thr Lys Ala Ala Glu Asp Gln Thr Ala Gln Val
    240                 245                 250
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ACG TTT ACG CGG AAC GGT GTC CTG GAT GAC GTT ACG GGT ATC 1098
Thr Phe Thr Arg Asn Gly Val Leu Asp Asp Val Thr Gly Ile
255 260 265

GTG GCC TGG GGC AAG TGG AAC GAA GCC AGC CAG AGC TAC AAG 1140
Val Ala Trp Gly Lys Trp Asn Glu Ala Ser Gln Ser Tyr Lys
270 275 280

GCT TTG ACT TCA CCA ACG ATT GCC GGC TAC GCG CCA AGC GAA 1182
Ala Leu Thr Ser Pro Thr Ile Ala Gly Tyr Ala Pro Ser Glu
285 290

GCG GTG GTA AAC CGC AGT TCC AAC AGC GAT GCC GAA CAA GGC 1224
Ala Val Val Asn Arg Ser Ser Asn Ser Asp Ala Glu Gln Gly
295 300 305

CCA ACG CTT ACC GTC ATT TAC ACG GCT GAT GCC CAA AAG GTT 1266
Pro Thr Leu Thr Val Ile Tyr Thr Ala Asp Ala Gln Lys Val
310 315 320

CAC GTT CAA TAC ATT GAT GGT GAA ACT GAC CAG ATG CTG CGT 1308
His Val Gln Tyr Ile Asp Gly Alu Thr Asp Gln Met Leu Arg
325 330 335

CAG GAT GAT TTG GAC GGC TAC ACG GAT GAA ACG ATT CCT TAC 1350
Gln Asp Asp Leu Asp Gly Tyr Thr Asp Glu Thr Ile Pro Tyr
340 345 350

AGC ACG GCT GAA GGC ATC AAG AAG TTT GAA GGC GAC GGT TAT 1392
Ser Thr Ala Glu Gly Ile Lys Lys Phe Glu Gly Asp Gly Tyr
355 360

GAA CTG TTC AAG GAC AAC TTC CCA GCT GGT GAG AAG TTC GAT 1434
Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly Glu Lys Phe Asp
365 370 375

AAC GAT GAC AAG AAT GAC CAA ACC TAC ACG GTA ATC TTC AAG 1476
Asn Asp Asp Lys Asn Asp Gln Thr Tyr Thr Val Ile Phe Lys
380 385 390

CAC CAT CGT GAA AAC GTT GAT CCA AAC CAC TCC TCG GCT GAT 1518
His His Arg Glu Asn Val Asp Pro Asn His Ser Ser Arg Asp
395 400 405

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GGC ACG AAG GGT ACG AAG ACC CTG ACG GAA ACG GTT CAC TAC      1560
Gly Thr Lys Gly Thr Lys Thr Leu Thr Glu Thr Val His Tyr
            410                 415                 420

AAG TAC GCA GAT GGT ACC AAG GCC GCT GAA GAT CAG ACG GCT      1602
Lys Tyr Ala Asp Gly Thr Lys Ala Ala Glu Asp Gln Thr Ala
                425                 430

CAG GTA ACG TTT ACG CGG AAC GGT GTC CTG GAT GAC GTT ACG      1644
Gln Val Thr Phe Thr Arg Asn Gly Val Leu Asp Asp Val Thr
435                 440                 445

GGT ATC GTG GCC TGG GGC AAG TGG AAC GAA GCC AGC CAG AGC      1686
Gly Ile Val Ala Trp Gly Lys Trp Asn Glu Ala Ser Gln Ser
    450                 455                 460

TAC AAG GCT TTG ACT TCA CCA ACG ATT GCC GGC TAC ACG CCA      1728
Tyr Lys Arg Leu Thr Ser Pro Thr Ile Ala Gly Tyr Thr Pro
        465                 470                 475

AGC GAA GCG GTG GTA AAG CGC AGT TCC AAC AGC GAT GCC GAA      1770
Ser Glu Ala Val Val Lys Arg Ser Ser Asn Ser Asp Ala Glu
            480                 485                 490

CAA GGC CCA ACG CTT ACG GTC ATC TAC ACG GCT GAT GCC CAA      1812
Gln Gly Pro Thr Leu Thr Val Ile Tyr Thr Ala Asp Ala Gln
                495                 500

AAG GTT CAC GTT CAA TAC ATT GAT GGT GAA ACT GAC CAG ATG      1854
Lys Val His Val Gln Tyr Ile Asp Gly Glu Thr Asp Gln Met
505                 510                 515

CTG CGT CAG GAT GAT TTG GAC GGC TAC ACG GAT GAA ACG ATT      1896
Leu Arg Gln Asp Asp Leu Asp Gly Tyr Thr Asp Gly Thr Ile
    520                 525                 530

CCT TAC AGC ACG GCT GAA GGC ATC AAG AAG TTT GAA GGC GAC      1938
Pro Tyr Ser Thr Ala Glu Gly Ile Lys Lys Phe Glu Gly Asp
        535                 540                 545

GGT TAT GAA CTG TTC AAG GAC AAC TTC CCA GCT GGT GAG AAG      1980
Asp Tyr Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly Glu Lys
            550                 555                 560

TTC GAT AAC GAT GAC ACC AAC GAT CAA TTC TAC ACG GTA ATC      2022
Phe Asp Asn Asp Asp Thr Asn Asp Gln Phe Tyr Thr Val Ile
                565                 570
```

```
TTC AAG CAC CAT CGT GAA AAC GTT GAT CCA AAC CAC TCC TCG      2064
Phe Lys His His Arg Glu Asn Val Asp Pro Asn His Ser Ser
575                 580                 585

GCT GAT GGC ACG AAG GGT ACG AAG ACG CTG ACG GAA ACG GTT      2106
Ala Asp Gly Thr Lys Gly Thr Lys Thr Leu Thr Glu Thr Val
    590                 595                 600

CAC TAC AAG TAC GCT AAT GGC ACC AAG GCG GCT GAA GAT CAG      2148
His Tyr Lys Tyr Ala Asn Gly Thr Lys Ala Ala Glu Asp Gln
        605                 610                 615

ACG GCT CAG GTA ACG TTT ACG CGG AAC GGT GTC CTG GAT GAC      2190
Thr Ala Gln Val Thr Phe Thr Arg Asn Gly Val Leu Asp Asp
            620                 625                 630

GTT ACG GGT ATC GTC GCC TGG GGC AAG TGG AAC GAA GCC AGC      2232
Val Thr Gly Ile Val Ala Trp Gly Lys Trp Asn Glu Ala Ser
                635                 640

CAG AGC TAC AAG GCT TTG ACT TCA CCA ACG ATT GCC GGC TAC      2274
Gln Ser Tyr Lys Ala Leu Thr Ser Pro Thr Ile Ala Gly Tyr
645                 650                 655

ACG CCA AGC GAA GCG GTG GTA AAG CGC AGT TCC AAC AGC GAT      2316
Thr Pro Ser Glu Ala Val Val Lys Arg Ser Ser Asn Ser Asp
    660                 665                 670

GCC GAA CAA GGC CCA ACG CTT ACG GTC ATC TAC ACG GCT GAT      2358
Ala Glu Gln Gly Pro Thr Leu Thr Val Ile Tyr Tht Ala Asp
        675                 680                 685

GCC CAA AAG GTT CAC GTT CAA TAC ATT GAT GGT GAA ACT GAC      2400
Ala Gln Lys Glu His Glu Gln Tyr Ile Asp Gly Glu Thr Asp
            690                 695                 700

CAG ATG CTG CGT CAG GAT GAT TTG GAC GGC TAC ACG GAT GAA      2442
Gln Met Leu Arg Gln Asp Asp Leu Asp Gly Tyr Thr Asp Glu
                705                 710

ACG ATT CCT TAC AGC ACG GCT GAA GGC ATC AAG AAG TTT GAA      2484
Thr Ile Pro Tyr Ser Thr Ala Glu Gly Ile Lys Lys Phe Glu
715                 720                 725
```

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GGC GAC GGT TAT GAA CTG TTC AAG GAC AAC TTC CCA GCT GGT      2526
Gly Asp Gly Tyr Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly
    730                 735                 740

GAG AAG TTC GAT AAC GAT GAC ACC AAC GAT CAT TCT ACA CGG      2568
Glu Lys Phe Asp Asn Asp Asp Thr Asn Asp His Ser Thr Arg
        745                 750                 755

TAT CTC AAG CCA CAT CGT GAA ACG TTG ATC CAA                  2601
Tyr Leu Lys Pro His Arg Glu Thr Leu Ile Gln
            760                 765
```

We claim:

1. A gene, *agg*, from *Lactobacillus reuteri* encoding a 60 kD protein mediating bacterial aggregation.

2. A DNA sequence as shown in Seq ID. No. 1.

3. An amino acid sequence as shown in Seq ID No. 1.

4. A gene, *muc*, from *L. reuteri* encoding a 200 kD protein that enhances binding to mucin.

5. The gene according to claim 4 wherein said mucin is present in the nasal passages or the gastrointestinal tract of an animal

6. A DNA sequence as shown in Seq ID No. 2.

7. An amino acid sequence as shown in Seq ID No. 2.

8. A method for expressing a heterologous antigen on the surface of a *Lactobacillus* cell comprising the steps of

   (a) fusing a heterologous gene in proper reading frame with a DNA sequence encoding a gene, *agg*, or a gene *muc* of a *Lactobacillus* species. the genes operably linked with a suitable promoter; and

   (b) transforming suitable host *Lactobacillus* cells with a hybrid plasmid vector comprising a fusion gene prepared in (a).

9. A method according to claim 8 wherein the host is *Lactobacillus reuteri*.

10. A method according to claim 8 wherein the heterologous gene is derived from a pathogenic microorganism.

11. A method according to claim 10 wherein the pathogenic microorganism is *E. coli*.

12. The method of claim 8 wherein the hybrid vector containing the fusion gene is integrated into the chromosome of the transformed host cell.

13. A non-virulent bacterial species expressing a heterologous antigen as a result of introducing into cells of the non-virulent species an expression cassette comprising DNA sequences encoding the heterologous antigen and a *Lactobacillus* gene selected from the group consisting of *agg* and *muc* under control of regulatory regions recognized by the cells of the non-virulent species.

14. A non-virulent bacterial species according to claim 13 wherein the species is *Lactobacillus*.

15. A non-virulent species according to claim 14 wherein the species is *Lactobacillus reuteri*.

16. A *Lactobacillus* species according to claim 14 wherein the heterologous antigen is derived from *E. coli*.

17. A *Lactobacillus* species according to claim 16 wherein the *E. coli* is enterotoxigenic.

18 A *Lactobacillus* species according to claim 16 wherein the *E. coli* is enteropathogenic.

19. A *Lactobacillus* species according to claim 16 wherein the heterologous antigen is a protein expressed in the fimbriae of *E. coli*.

20. A *Lactobacillus* species according to claim 19 wherein the heterologous antigen is K88.

21. A method for vaccinating an animal comprising the steps of:

(a) identifying and selecting species of *Lactobacilli* displaying desirable characteristics for targeting and adhering to mucosal tissue;

(b) identifying and selecting strains of *Lactobacilli* additionally demonstrating the potential to express heterologous proteins;

(c) identifying and isolating the gene or genes encoding heterologous antigens derived from a pathogenic microorganism or from other biological material;

(d) fusing the genes of step (c) with a gene selected from the group consisting of *agg* and *muc* into an appropriate expression cassette containing regulatory regions recognized by *Lactobacilli*;

(e) transferring the expression cassette into selected cells of *Lactobacilli* to form transformed *Lactobacilli*;

(f) selecting and growing transformed cells of *Lactobacilli* that can replicate and express on the cell surface antigenic proteins encoded by the inserted gene sequences;

(g) combining the modified *Lactobacilli* cells with pharmaceutically acceptable carriers to form a vaccine; and

(h) administering the oral vaccine to an animal recipient.

22. The method of claim 21 additionally comprising the step of administering to the animal antibiotics to eradicate transformed *Lactobacilli* after colonization.

23. A method according to claim 21 wherein the pathogenic microorganism is an *E. coli* strain.

24. A method according to claim 23 wherein the *E. coli* strain is an enterotoxigenic *E. coli*.

25. A method according to claim 23 wherein the *E. coli* strain is an enteropathogenic *E. coli*.

26. A method according to claim 23 wherein the antigen is expressed in the fimbriae of *E. coli*.

27. A method according to claim 26 wherein the fimbriae antigen is K88.

28. A method according to claim 21 wherein the *Lactobacilli* are *L. reuteri*.

29. A method for preventing or treating infections of mammalian mucous membranes by pathogenic microorganisms the method comprising enteral administration of a vaccine prepared according to the method of claim 21.

30. The vaccine of claim 29 wherein the pharmaceutically acceptable carrier is a milk product.

31. The method according to claim 29 wherein said mammalian mucous membranes are located in the nasopharynx, pharynx, esophagus, stomach, small intestine and large intestine.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Casas, Ivan
Jonsson, Hans
Möllstam, Bo
Roos, Stefan

(ii) TITLE OF INVENTION: Lactobacilli Harboring Aggregation and Mucin Binding Genes As Vaccine Delivery Vehicles

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Dublin

(D) STATE: Ohio

(E) COUNTRY: US

(F) ZIP: 43017

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44Mb storage

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: MS-DOS Version 6.22

(D) SOFTWARE: Microsoft Word Version 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/039,773

(B) FILING DATE: 16-MAR-1998

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA: Not applicable

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Donald O. Nickey

(B) REGISTRATION NUMBER: 29,092

(C) REFERENCE/DOCKET NUMBER: 1229-005

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(B) TELEFAX: (614) 792-5536

(C) TELEX: Not applicable

(2) INFORMATION FOR SEQUENCE ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Genomic DNA

(A) DESCRIPTION: Genomic DNA sequence and deduced amino acid sequence of bacterial aggregation protein

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus reuteri* sp

(B) STRAIN: 1063

(C) CELL TYPE: Unicellular organism

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1

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ATTAATTGCC GATCTTACGG CTACTTTGAC AGGTGAGGAT ATTGTTCTAT        50

TGAAAGCAAG CCATGGTATT CACCTAGAAG AAGTCTTGAC GGCATTAAAA       100

GCAGAATAGT TAATATATTT GCCAGTCGAT TACTGATGCT TATATCATGA       150

ATCGACTGGT CATTTTTAGG AGGAAAATTT TTG AAG TTT AGT GAA TTA     198
                                 Met Lys Phe Ser Glu Leu
                                  1               5

GGC TTA TCC GAT AGC CTA TTA AAA GCA ATC AAA CGG AGC GGA      240
Gly Leu Ser Asp Ser Leu Leu Lys Ala Ile Lys Arg Ser Gly
            10                  15                  20

TAC GAA GAA GCA ACA CCA ATT CAA GAA CAA ACG ATT CCA ATG      282
Tyr Glu Glu Ala Thr Pro Ile Gln Glu Gln Thr Ile Pro Met
                25                  30

GTT CTT GAG GGT AAG GAT GTT ATT GGT CAA GCA CAG ACT GGA      324
Val Leu Glu Gly Lys Asp Val Ile Gly Gln Ala Gln Thr Gly
 35                  40                  45

ACT GGT AAG ACG GCT GCT TTT GGG TTG CCA ATT ATT GAA AAC      366
Thr Gly Lys Thr Ala Ala Phe Gly Leu Pro Ile Ile Glu Asn
     50                  55                  60

GTT GAT ACT GAA AAT CCC AAT ATT CAA GCA ATT ATC ATT TCA      408
Val Asp Thr Glu Asn Pro Asn Ile Gln Ala Ile Ile Ile Ser
         65                  70                  75

CCA ACA CGT GAA TTA GCG ATC CAG ACC CAA GAA GAA CTT TAT      450
Pro Thr Arg Glu Leu Als Ile Gln Thr Gln Glu Glu Leu Tyr
             80                  85                  90

CGT CTA GGT AAA GAT AAA CAT GTT CGC GTG CAG GTA GTC TAT      492
Arg Leu Gly Lys Asp Lys His Val Arg Val Gln Val Val Tyr
                 95                 100

GGT GGG GCA GAT ATT CGG CGC CAA ATT AAG AGC TTG AAA CAA      534
Gly Gly Ala Asp Ile Arg Agr Gln Ile Lys Ser Leu Lys Gln
105                 110                 115

CAC CCC CAA ATT CTC GTG GGG ACC CCT GGA CGG TTA CGT GAC      576
His Pro Gln Ile Leu Val Gly Thr Pro Gly Arg Leu Arg Asp
     120                 125                 130
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CAT ATT AAC CGT CAT ACA GTT AAA CTT GAC CAC ATT AAG ACC      618
His Ile Asn Arg His Thr Val Lys Leu Asp His Ile Lys Thr
        135                 140                 145

CTG GTT CTC GAT GAA GCA GAT GAA ATG CTA AAC ATG GGA TTC      660
Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe
            150                 155                 160

TTA GAA GAT ATT GAA TCC ATC ATC AAG GAA ACA CCA GAT GAT      702
Leu Glu Asp Ile Glu Ser Ile Ile Lys Glu Thr Pro Asp Asp
                165                 170

CGG CAA ACT TTG CTC TTC TCA GCA ACC ATG CCA CCA GAA ATC      744
Arg Gln Thr Leu Leu Phe Ser Ala Thr Met Pro Pro Glu Ile
175                 180                 185

AAG CGA ATT GGG GTT CAA TTT ATG TCT GAT CCG GAA ACT GTG      786
Lys Arg Ile Gly Val Gln Phe Met Ser Asp Pro Glu Thr Val
    190                 195                 200

CGG ATC AAG GCC AAG GAA TTG ACT ACT GAC TTA GTT GAT CAG      828
Arg Ile Lys Ala Lys Glu Leu Thr Thr Asp Leu Val Asp Gln
        205                 210                 215

TAC TAT GTT CGC GCT CGT GAC TAT GAA AAG TTT GAC ATC ATG      870
Tyr Tyr Val Arg Ala Arg Asp Tyr Glu Lys Phe Asp Ile Met
            220                 225                 230

ACC CGC TTA ATT GAT GTT CAA GAT CCT GAC TTA ACA ATT GTC      912
Thr Arg Leu Ile Asp Val Gln Asp Pro Asp Leu Thr Ile Val
                235                 240

TTT GGT CGG ACA AAG CGG CGG GTA GAT GAA TTG TCG AAG GGC      954
Phe Gly Arg Thr Lys Arg Arg Val Asp Glu Leu Ser Lys Gly
245                 250                 255

TTG ATT GCG CGT GGC TAC AAT GCA GCT GGT ATC CAT GGT GAC      996
Leu Ile Ala Arg Gly Tyr Asn Ala Ala Gly Ile His Gly Asp
    260                 265                 270

CTT ACT CAG GAT AAG CGT TCT AAG ATC ATG TGG AAG TTT AAG     1038
Leu Thr Gln Asp Lys Arg Ser Lys Ile Met Trp Lys Phe Lys
        275                 280                 285

AAC AAT GAA CTT GAT ATC TTA GTT GCA ACA GAT GTG GCT GCC     1080
Asn Asn Gly Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala
            290                 295                 300
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CGG GGC TTA GAC ATT TCG GGG GTT ACG CAT GTT TAT AAT TAT     1122
Arg Gly Leu Asp Ile Ser Gly Val Thr His Val Tyr Asn Tyr
                305                 310

GAT ATT CCA TCT GAC CCA GAC AGC TAT GTT CAC CGG ATT GGC     1164
Asp Ile Pro Ser Asp Pro Asp Ser Tyr Val His Arg Ile Gly
315                 320                 325

CGA ACA GGA CGG GCC GGA CAT CAC GGG GTA TCT TTA ACC TTT     1206
Arg Thr Gly Arg Ala Gly His His Gly Val Ser Leu Thr Phe
    330                 335                 340

GTG ACT CCA AAT GAG ATG GAT TAC CTT CAT GAG ATT GAA AAA     1248
Val Thr Pro Asn Glu Met Asp Tyr Leu His Glu Ile Gly Lys
        345                 350                 355

TTA ACC CGG GTA CGG ATG TTG CCA CTC AAG CCA CCA ACA GCT     1290
Leu Thr Arg Val Arg Met Leu Pro Leu Lys Pro Pro Thr Ala
            360                 365                 370

GAA GAA GCA TTT AAG GGT CAA GTA GCA TCG GCC TTT AAT GAT     1332
Glu Glu Ala Phe Lys Gly Gln Val Ala Ser Ala Phe Asn Asp
                375                 380

ATC GAT GAA TTA ATC GCG CAG GAT TCA ACT GAT CGT TAT GAA     1374
Ile Asp Glu Leu Ile Ala Gln Asp Ser Thr Asp Arg Tyr Glu
385                 390                 395

GAA GCC GCT GAA AAG CTA TTA GAA ACT CAT AAT GCA ACT GAC     1416
Glu Ala Ala Glu Lys Leu Leu Glu Thr His Asn Ala Thr Asp
    400                 405                 410

CTA GTA GCA GCA TTG TTA AAT AAC ATG ACG AAG GAA GCA GCG     1458
Leu Val Ala Ala Leu Leu Asn Ans Met Thr Lys Glu Ala Ala
        415                 420                 425

AGT GAG GTT CCC GTT AAG ATT ACC CCT GAG CGT CCC CTT CCA     1500
Ser Glu Val Pro Val Lys Ile Thr Pro Glu Arg Pro Leu Pro
            430                 435                 440
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CGG CGT AAT AAG CGG AAT AAC CGT AAT GGC AAC CGC AAT AAC    1542
Arg Arg Asn Lys Arg Asn Asn Arg Asn Gly Asn Arg Asn Asn
                445                 450

TCG CAT GGT GGC AAC CAC TAC CGG CGT AAG AAT TTC CGT CGT    1584
Ser His Gly Gly Asn His Tyr Arg Arg Lys Asn Phe Arg Arg
455                 460                 465

CAC CAA CAT GGC AGT CAT CGA AAT GAT AAC CAT GGG AAG AGC    1626
His Gln His Gly Ser His Arg Asn Asp Asp His Gly Lys Ser
    470                 475                 480

CAT TCC AGT CGT CAT TCA TTT AAT ATT CGG CAC CGG AAA GAA    1668
His Ser Ser Arg His Ser Phe Asn Ile Arg His Arg Lys Gly
        485                 490                 495

AAT TAA TTA TGA AGCCTTTGGT TGTGACGTGT ACCCTTAAAG           1710
Asn

TTGGAACTTG TATGTTCTTA CTTGTAAATT GAATAATTAT                1750

TTTTCTTAGG CAACTAAATT CTGCTCGTAT TGGAGTGGTG TTTGGTTGCC     1800
```

(2) INFORMATION FOR SEQUENCE ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2601 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Genomic DNA

(A) DESCRIPTION: Partial genomic DNA sequence and deduced amino acid sequence of mucin binding protein

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus reuteri* sp

(B) STRAIN: 1063

(C) CELL TYPE: Unicelluar organism

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2

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ATGATGTTCA ACAATTGGTT AAAGCTGCCA TTGAGTTAGG TGTCCAAATA      50

GACTTGCAAC CAACGCAAGT AGTATTATAT GTAGGAGATC ATCAAGAAAG     100

CTATAATGCT CAAGCAACTT TTGATTTCTC AAAGGGTGCT CGTGATGTAA     150

TTCTTAGTGA TTTTCCAGAA GTTCAGGATT TTCAGGAAAA GTAAAAAAGA     200

GACTGAGGAG ATTATTTCCT AGTCTCTATC TTTTTAAAGT AGGGTAATAA     250

CCTTGTTTTC ACTTTCGTTA TTTCCCGGGA AATAGAAAGA AGCGCTAAAA     300

ATG AGA AAG ATT GGA ATT GTT GGC CTC GGT CAT GTG GGT GAA     342
Met Arg Lys Ile Gly Ile Val Gly Leu Gly His Val Gly Glu
 1               5                  10

ATG CTA GCC AAC CAA TTA GTA ATG AAC GGA AAA GTT GAT GAA     384
Met Leu Ala Asn Gln Leu Val Met Asn Gly Lys Val Asp Glu
 15                  20                  25

TTA GTT TTG ATT GAT GAA AAA GAT CCA CAA AAA GGT CAA AAG     426
Leu Val Leu Ile Asp Glu Lys Asp Pro Gln Lys Gly Gln Lys
     30                  35                  40

ACG GTT ACA CAG ACA ATT AAG TAC GAA TAC GCT GAT GGC ACG     468
Thr Val Thr Gln Thr Ile Lys Tyr Glu Tyr Ala Asp Gly Thr
         45                  50                  55

GCA ACT GGT TTG GCT GAT AAT GTG CAA ACC TTG ACG TTC AAG     510
Ala Thr Gly Leu Ala Asp Asn Val Gln Thr Leu Thr Phe Lys
             60                  65                  70

CGT ACA GGT GAC AAG GAT CTC GTT ACT CAT GAA GTA ACC TGG     552
Arg Thr Gly Asp Lys Asp Leu Val Thr His Glu Val Thr Trp
                 75                  80
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CCA GAC TGG TCA ACG GTT GCC GGT CAA CAA ACC AGT GTT GTA        594
Pro Asp Trp Ser Thr Val Ala Gly Gln Gln Thr Ser Val Val
 85                 90                  95

ACC AGT CCA GCT CTC AAG GGC TAC ACT GCT GAT ACC AAC GAA        636
Thr Ser Pro Ala Leu Lys Gly Tyr Thr Ala Asp Thr Asn Glu
    100                 105                 110

ATT CCA GCC ATT ACC TAC CAT GCT GGT GAC AGT GAT GTT ACT        678
Ile Pro Ala Ile Thr Tyr His Ala Gly Asp Ser Asp Val Thr
        115                 120                 125

TAT GTT GTT AAG TAC AAT GCC GAT GTT CAA CAT GCT GTT ATC        720
Tyr Val Val Lys Tyr Asn Ala Asp Val Gln His Ala Val Ile
            130                 135                 140

AAT TAC ATT GAT GGC GAA AGT GAT GAG ATA CTG CAC ACT GAT        762
Asn Tyr Ile Asp Gly Glu Ser Asp Glu Ile Leu His Thr Asp
                145                 150

AAG GTT AAT GGC CAC TCT GAC GAA AAG ATC AAC TAC AGC ACT        804
Lys Val Asn Gly His Ser Asp Glu Lys Ile Asn Tyr Ser Thr
155                 160                 165

GCT GAT ATG ATC AAA CAG TTG GAA GCC AAG GGT TAT GAA CTG        846
Ala Asp Met Ile Lys Gln Leu Glu Ala Lys Gly Tyr Glu Leu
    170                 175                 180

TTC AAG GAC AAC TTC CCA GCT GGT GAG AAG TTC GAT AAC GAT        888
Phe Lys Asp Asn Phe Pro Ala Gly Glu Lys Phe Asp Asn Asp
        185                 190                 195

GAC ACC AAC GAT CAA TTC TAC ACG GTA ATC TTC AAG CAC CAT        930
Asp Thr Asn Asp Gln Phe Tyr Thr Val Ile Phe Lys His His
            200                 205                 210

CGT GAA AAC GTT GAT CCA AAC CAC TCC TCG GCT GAT GGC ACG        972
Arg Glu Asn Val Asp Pro Asn His Ser Ser Ala Asp Gly Thr
                215                 220

AAG GGT ACG AAG ACG CTG ACG GAA ACG GTT CAC TAC AAG TAC       1014
Lys Gly Thr Lys Thr Leu Thr Glu Thr Val His Tyr Lys Tyr
225                 230                 235

GCT AAT GGC ACC AAG GCG GCT GAA GAT CAG ACG GCT CAG GTA       1056
Ala Asn Gly Thr Lys Ala Ala Glu Asp Gln Thr Ala Gln Val
    240                 245                 250
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ACG TTT ACG CGG AAC GGT GTC CTG GAT GAC GTT ACG GGT ATC      1098
Thr Phe Thr Arg Asn Gly Val Leu Asp Asp Val Thr Gly Ile
        255                 260                 265

GTG GCC TGG GGC AAG TGG AAC GAA GCC AGC CAG AGC TAC AAG      1140
Val Ala Trp Gly Lys Trp Asn Glu Ala Ser Gln Ser Tyr Lys
            270                 275                 280

GCT TTG ACT TCA CCA ACG ATT GCC GGC TAC GCG CCA AGC GAA      1182
Ala Leu Thr Ser Pro Thr Ile Ala Gly Tyr Ala Pro Ser Glu
                285                 290

GCG GTG GTA AAC CGC AGT TCC AAC AGC GAT GCC GAA CAA GGC      1224
Ala Val Val Asn Arg Ser Ser Asn Ser Asp Ala Glu Gln Gly
295                 300                 305

CCA ACG CTT ACC GTC ATT TAC ACG GCT GAT GCC CAA AAG GTT      1266
Pro Thr Leu Thr Val Ile Tyr Thr Ala Asp Ala Gln Lys Val
    310                 315                 320

CAC GTT CAA TAC ATT GAT GGT GAA ACT GAC CAG ATG CTG CGT      1308
His Val Gln Tyr Ile Asp Gly Alu Thr Asp Gln Met Leu Arg
        325                 330                 335

CAG GAT GAT TTG GAC GGC TAC ACG GAT GAA ACG ATT CCT TAC      1350
Gln Asp Asp Leu Asp Gly Tyr Thr Asp Glu Thr Ile Pro Tyr
            340                 345                 350

AGC ACG GCT GAA GGC ATC AAG AAG TTT GAA GGC GAC GGT TAT      1392
Ser Thr Ala Glu Gly Ile Lys Lys Phe Glu Gly Asp Gly Tyr
                355                 360

GAA CTG TTC AAG GAC AAC TTC CCA GCT GGT GAG AAG TTC GAT      1434
Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly Glu Lys Phe Asp
365                 370                 375

AAC GAT GAC AAG AAT GAC CAA ACC TAC ACG GTA ATC TTC AAG      1476
Asn Asp Asp Lys Asn Asp Gln Thr Tyr Thr Val Ile Phe Lys
    380                 385                 390

CAC CAT CGT GAA AAC GTT GAT CCA AAC CAC TCC TCG GCT GAT      1518
His His Arg Glu Asn Val Asp Pro Asn His Ser Ser Arg Asp
        395                 400                 405
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GGC ACG AAG GGT ACG AAG ACC CTG ACG GAA ACG GTT CAC TAC 1560
Gly Thr Lys Gly Thr Lys Thr Leu Thr Glu Thr Val His Tyr
410 415 420

AAG TAC GCA GAT GGT ACC AAG GCC GCT GAA GAT CAG ACG GCT 1602
Lys Tyr Ala Asp Gly Thr Lys Ala Ala Glu Asp Gln Thr Ala
425 430

CAG GTA ACG TTT ACG CGG AAC GGT GTC CTG GAT GAC GTT ACG 1644
Gln Val Thr Phe Thr Arg Asn Gly Val Leu Asp Asp Val Thr
435 440 445

GGT ATC GTG GCC TGG GGC AAG TGG AAC GAA GCC AGC CAG AGC 1686
Gly Ile Val Ala Trp Gly Lys Trp Asn Glu Ala Ser Gln Ser
450 455 460

TAC AAG GCT TTG ACT TCA CCA ACG ATT GCC GGC TAC ACG CCA 1728
Tyr Lys Arg Leu Thr Ser Pro Thr Ile Ala Gly Tyr Thr Pro
465 470 475

AGC GAA GCG GTG GTA AAG CGC AGT TCC AAC AGC GAT GCC GAA 1770
Ser Glu Ala Val Val Lys Arg Ser Ser Asn Ser Asp Ala Glu
480 485 490

CAA GGC CCA ACG CTT ACG GTC ATC TAC ACG GCT GAT GCC CAA 1812
Gln Gly Pro Thr Leu Thr Val Ile Tyr Thr Ala Asp Ala Gln
495 500

AAG GTT CAC GTT CAA TAC ATT GAT GGT GAA ACT GAC CAG ATG 1854
Lys Val His Val Gln Tyr Ile Asp Gly Glu Thr Asp Gln Met
505 510 515

CTG CGT CAG GAT GAT TTG GAC GGC TAC ACG GAT GAA ACG ATT 1896
Leu Arg Gln Asp Asp Leu Asp Gly Tyr Thr Asp Gly Thr Ile
520 525 530

CCT TAC AGC ACG GCT GAA GGC ATC AAG AAG TTT GAA GGC GAC 1938
Pro Tyr Ser Thr Ala Glu Gly Ile Lys Lys Phe Glu Gly Asp
535 540 545

GGT TAT GAA CTG TTC AAG GAC AAC TTC CCA GCT GGT GAG AAG 1980
Asp Tyr Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly Glu Lys
550 555 560

TTC GAT AAC GAT GAC ACC AAC GAT CAA TTC TAC ACG GTA ATC 2022
Phe Asp Asn Asp Asp Thr Asn Asp Gln Phe Tyr Thr Val Ile
565 570

TTC AAG CAC CAT CGT GAA AAC GTT GAT CCA AAC CAC TCC TCG 2064
Phe Lys His His Arg Glu Asn Val Asp Pro Asn His Ser Ser
575 580 585

GCT GAT GGC ACG AAG GGT ACG AAG ACG CTG ACG GAA ACG GTT 2106
Ala Asp Gly Thr Lys Gly Thr Lys Thr Leu Thr Glu Thr Val
590 595 600

CAC TAC AAG TAC GCT AAT GGC ACC AAG GCG GCT GAA GAT CAG 2148
His Tyr Lys Tyr Ala Asn Gly Thr Lys Ala Ala Glu Asp Gln
605 610 615

ACG GCT CAG GTA ACG TTT ACG CGG AAC GGT GTC CTG GAT GAC 2190
Thr Ala Gln Val Thr Phe Thr Arg Asn Gly Val Leu Asp Asp
620 625 630

GTT ACG GGT ATC GTC GCC TGG GGC AAG TGG AAC GAA GCC AGC 2232
Val Thr Gly Ile Val Ala Trp Gly Lys Trp Asn Glu Ala Ser
635 640

CAG AGC TAC AAG GCT TTG ACT TCA CCA ACG ATT GCC GGC TAC 2274
Gln Ser Tyr Lys Ala Leu Thr Ser Pro Thr Ile Ala Gly Tyr
645 650 655

ACG CCA AGC GAA GCG GTG GTA AAG CGC AGT TCC AAC AGC GAT 2316
Thr Pro Ser Glu Ala Val Val Lys Arg Ser Ser Asn Ser Asp
660 665 670

GCC GAA CAA GGC CCA ACG CTT ACG GTC ATC TAC ACG GCT GAT 2358
Ala Glu Gln Gly Pro Thr Leu Thr Val Ile Tyr Tht Ala Asp
675 680 685

GCC CAA AAG GTT CAC GTT CAA TAC ATT GAT GGT GAA ACT GAC 2400
Ala Gln Lys Glu His Glu Gln Tyr Ile Asp Gly Glu Thr Asp
690 695 700

CAG ATG CTG CGT CAG GAT GAT TTG GAC GGC TAC ACG GAT GAA 2442
Gln Met Leu Arg Gln Asp Asp Leu Asp Gly Tyr Thr Asp Glu
705 710

ACG ATT CCT TAC AGC ACG GCT GAA GGC ATC AAG AAG TTT GAA 2484
Thr Ile Pro Tyr Ser Thr Ala Glu Gly Ile Lys Lys Phe Glu
715 720 725

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GGC GAC GGT TAT GAA CTG TTC AAG GAC AAC TTC CCA GCT GGT        2526
Gly Asp Gly Tyr Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly
    730                 735                     740

GAG AAG TTC GAT AAC GAT GAC ACC AAC GAT CAT TCT ACA CGG        2568
Glu Lys Phe Asp Asn Asp Asp Thr Asn Asp His Ser Thr Arg
        745                 750                     755

TAT CTC AAG CCA CAT CGT GAA ACG TTG ATC CAA                    2601
Tyr Leu Lys Pro His Arg Glu Thr Leu Ile Gln
            760                 765
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